
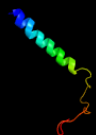







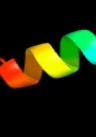







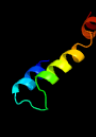

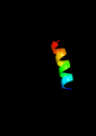




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2197c_(-)_2461512_2462156
Date	Mon Aug 5 13:25:32 BST 2019
Unique Job ID	1fd480e41c6ef730

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mk7F_	 Alignment		54.6	18	PDB header: oxidoreductase Chain: F: PDB Molecule: cytochrome c oxidase, cbb3-type, subunit p; PDBTitle: the structure of cbb3 cytochrome oxidase
2	d2i9wa1	 Alignment		27.2	36	Fold: Cystatin-like Superfamily: NTF2-like Family: SEC-C associated NTF2-like domain
3	c2jq5A_	 Alignment		24.8	55	PDB header: structural genomics Chain: A: PDB Molecule: sec-c motif; PDBTitle: solution structure of rpa3114, a sec-c motif containing protein from2 rhodopseudomonas palustris; northeast structural genomics consortium3 target rpt5 / ontario center for structural proteomics target rp3097
4	c2i9waA_	 Alignment		24.8	36	PDB header: metal binding protein Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a sec-c motif containing protein (psyc_2064) from2 psychrobacter arcticus at 1.75 a resolution
5	c5djqp_	 Alignment		15.0	62	PDB header: oxidoreductase Chain: P: PDB Molecule: putative uncharacterized protein; PDBTitle: the structure of cbb3 cytochrome oxidase.
6	c5djqn_	 Alignment		15.0	62	PDB header: oxidoreductase Chain: N: PDB Molecule: putative uncharacterized protein; PDBTitle: the structure of cbb3 cytochrome oxidase.
7	c5djqO_	 Alignment		15.0	62	PDB header: oxidoreductase Chain: Q: PDB Molecule: putative uncharacterized protein; PDBTitle: the structure of cbb3 cytochrome oxidase.
8	c5djqO_	 Alignment		15.0	62	PDB header: oxidoreductase Chain: O: PDB Molecule: putative uncharacterized protein; PDBTitle: the structure of cbb3 cytochrome oxidase.
9	c4dwlA_	 Alignment		14.4	33	PDB header: nucleic acid binding protein Chain: A: PDB Molecule: bbp7; PDBTitle: avd molecule from bordetella bacteriophage dgr
10	c3kdrC_	 Alignment		13.8	56	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hk97 family phage portal protein; PDBTitle: the crystal structure of a hk97 family phage portal protein from2 corynebacterium diphtheriae to 2.9a
11	c3kj0B_	 Alignment		13.1	55	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: mcl-1 in complex with bim bh3 mutant i2dy

12	c6btmC_	Alignment		12.5	22	PDB header: membrane protein Chain: C: PDB Molecule: alternative complex iii subunit c; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
13	c3iwdC_	Alignment		12.1	22	PDB header: lyase Chain: C: PDB Molecule: s-adenosylmethionine decarboxylase; PDBTitle: t. maritima adometdc complex with 5'-deoxy-5'-dimethyl thioadenosine
14	d1luxda_	Alignment		11.9	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
15	c5f5uE_	Alignment		9.5	44	PDB header: splicing Chain: E: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the snu23-prp38-mfap1(217-258) complex of2 chaetomium thermophilum
16	c4q2sA_	Alignment		9.1	35	PDB header: rna binding protein Chain: A: PDB Molecule: pdc1 ge1 domain; PDBTitle: crystal structure of s. pombe pdc1 ge1 domain
17	c6f0kC_	Alignment		8.9	17	PDB header: membrane protein Chain: C: PDB Molecule: polysulphide reductase nrfd; PDBTitle: alternative complex iii
18	c5f5uB_	Alignment		8.4	44	PDB header: splicing Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the snu23-prp38-mfap1(217-258) complex of2 chaetomium thermophilum
19	c4ojkC_	Alignment		7.8	31	PDB header: hydrolase/protein binding Chain: C: PDB Molecule: cgmp-dependent protein kinase 2; PDBTitle: structure of the cgmp dependent protein kinase ii and rab11b complex
20	c2ksdA_	Alignment		7.7	50	PDB header: transferase Chain: A: PDB Molecule: aerobic respiration control sensor protein arcb; PDBTitle: backbone structure of the membrane domain of e. coli histidine kinase2 receptor arcb, center for structures of membrane proteins (csm)3 target 4310c
21	c5f5uH_	Alignment	not modelled	7.1	44	PDB header: splicing Chain: H: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the snu23-prp38-mfap1(217-258) complex of2 chaetomium thermophilum
22	c2mxdA_	Alignment	not modelled	6.9	50	PDB header: viral protein Chain: A: PDB Molecule: viral protein genome-linked; PDBTitle: solution structure of vpg of porcine sapovirus
23	c3eyeA_	Alignment	not modelled	6.9	22	PDB header: transferase Chain: A: PDB Molecule: pts system n-acetylgalactosamine-specific iib component 1; PDBTitle: crystal structure of pts system n-acetylgalactosamine-specific iib2 component 1 from escherichia coli
24	c2b68A_	Alignment	not modelled	6.7	67	PDB header: antimicrobial protein Chain: A: PDB Molecule: defensin; PDBTitle: solution structure of the recombinant crassostrea gigas2 defensin
25	c2okrC_	Alignment	not modelled	6.4	38	PDB header: transferase Chain: C: PDB Molecule: map kinase-activated protein kinase 2; PDBTitle: crystal structure of the p38a-mapkap kinase 2 heterodimer
26	c3mp7B_	Alignment	not modelled	6.1	37	PDB header: protein transport Chain: B: PDB Molecule: preprotein translocase subunit sece; PDBTitle: lateral opening of a translocon upon entry of protein suggests the2 mechanism of insertion into membranes
27	c2okrF_	Alignment	not modelled	6.0	38	PDB header: transferase Chain: F: PDB Molecule: map kinase-activated protein kinase 2; PDBTitle: crystal structure of the p38a-mapkap kinase 2 heterodimer
28	c5f5tD_	Alignment	not modelled	5.8	44	PDB header: splicing Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the prp38-mfap1 complex of chaetomium2 thermophilum

29	c1wlpA_	Alignment	not modelled	5.4	27	PDB header: oxidoreductase/signaling protein Chain: A: PDB Molecule: cytochrome b-245 light chain; PDBTitle: solution structure of the p22phox-p47phox complex
30	c4hg6B_	Alignment	not modelled	5.3	19	PDB header: transferase Chain: B: PDB Molecule: cellulose synthase subunit b; PDBTitle: structure of a cellulose synthase - cellulose translocation2 intermediate
31	c6ge2A_	Alignment	not modelled	5.2	38	PDB header: hormone Chain: A: PDB Molecule: exendin-4; PDBTitle: exendin-4 based dual glp-1/glucagon receptor agonist
32	d1blea_	Alignment	not modelled	5.1	22	Fold: PTS IIb component Superfamily: PTS IIb component Family: PTS IIb component